2/3

ATOGOTICOTTIGICACTOSOCICAGOSTGGCCCTTAGOTICATCGCCCTAGCTGGCTGGCTTCTCCATTTACCAGAA 80 MASFVIRESLALSFIALAGESIYON TACCCATACAGCCATGAAAGGGCAGCTTAAGCTCACCCCAAAGTGGCTGCTAGACAACACTCTAGAGTGGTCAGTUGCCG 160 THTARKGOLKLIPKWILDRILESSVA

FIG. 1b

ACSTRUCTCICACTAGSCCTAGSCATCTCCTCCGGCGAAGGCTTTCCGGCGAGGACGGCAFAITCTCCGCCD V L S L R L G I S S G K L S D E D C I F S A		240
STORACOCCOCCATEGATGCAGAAACCOCCATGGGTGCTTCCCCTCATTCCCCTCTTCTCCATGACT		320
ACETACGCTAATTTTGTACGATBATGTTTTTTTTTTTTTTTTT	GAAATTAAACAGA	400
TTGAAATGTGTGTTATTAATGTATTATCTGCAGGGTTGTGAGGGAGG		480
AGA/CAGACGCCGCCA/TAA/TAACTCAGTCAGACGTTTTGAGGTGATACAACAAGCTAAAGAG E Q F A G S N N N S V T G F E V I Q Q A K E N		560
ANTIGUED ACATACAAG FARCTIGUEGEGACATCHTATECATTECTCCCCGFGATTCTTTCCAGAGCC PYIQVS CADILSIAARDS FQR	AGTAAGTCCATTT	640
ATTTCTAAAGGTTGAAATTAATAAGAACAAGAATCCAAACAAA	TTATGTGGTTTGA	720
CARTATGUTGAAATTGUTTTATATTAATGACTAGTATTTATGCATTATATTTATATGCAACTCTA	AACATRICAGTITIA F	800
CTGGAGAAACGTACACGGTGACTCTGGGAGAACTCGATGCAAGAACGGGAGACTTACCGGAGCTAAT G E I Y I V I Ł G R Ł D A R I A N Ł I S A N		880
$\begin{array}{llllllllllllllllllllllllllllllllllll$		960
AGGICTICACACGGTTGGGTTTTCGAGATGTCCGCTTTTATGCGTTCCCATTTTCATCATCCCGCC		1040
TGCAATGCAACTGTCCGGTGGGGCCGGGCCCGACTCCGTTGACCLL Q C N C P V S P D D T G L V G L D P T P L T		1120
TITTACTOCOGACOTGOCIAACGGACAAGGGCTTCTCTCCGACAACGAGCTGATGAATAGCAACAGF Y S D V A N G Q G L L F S D N E L N N S N T		1200
CCTTAGGAGGTACAGGGAGAGAGAGAGGCTTTTCTCSCCCGATTTCCCCCGCCCATGGTGAACATG V R R Y R D E M D A F L A D F A A A M V K M		1280
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$		1360
TICCCATOBACATCAATAAOSTCTGTGATTCTGTGAAAGTTTTACTGGGACTGTGAAGAATTTTCAC	THETOTISTITE	1440
TGAAATAAAAAAAAATTTTTTTTATGTCCTAACAAAACTTGTATTACTGAATAAAATTTATAAATT	TGTTA	1512
2	(SEQ ID I	NO:1